



OIKE

RAW SEQUENCE LISTING

DATE: 01/23/2002

PATENT APPLICATION: US/09/766,678

TIME: 10:05:23

Input Set : N:\Crf3\RULE60\09766678.raw.txt

Output Set: N:\CRF3\01232002\I766678.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Ullrich, Axel

6 Risau, Werner

7 Millauer, Birgit

8 Gazit, Aviv

9 Levitzki, Alex

11 (ii) TITLE OF INVENTION: Flk-1 Is A Receptor For Vascular

12 Endothelial Growth Factor

14 (iii) NUMBER OF SEQUENCES: 6

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: Pennie & Edmonds

18 (B) STREET: 1155 Avenue of the Americas

19 (C) CITY: New York

20 (D) STATE: New York

21 (E) COUNTRY: U.S.A.

22 (F) ZIP: 10036-2711

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk

26 (B) COMPUTER: IBM PC compatible

27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/09/766,678

C--> 32 (B) FILING DATE: 25-Jan-2001

33 (C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: 08/193,829

37 (B) FILING DATE: 09-FEB-1994

40 (viii) ATTORNEY/AGENT INFORMATION:

41 (A) NAME: Coruzzi, Laura A.

42 (B) REGISTRATION NUMBER: 30,742

43 (C) REFERENCE/DOCKET NUMBER: 7683-060

45 (ix) TELECOMMUNICATION INFORMATION:

46 (A) TELEPHONE: (212)790-9090

47 (B) TELEFAX: (212)869-9741

48 (C) TELEX: 66141 PENNIE

51 (2) INFORMATION FOR SEQ ID NO: 1:

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 5470 base pairs

55 (B) TYPE: nucleic acid

56 (C) STRANDEDNESS: unknown

57 (D) TOPOLOGY: unknown

ENTERED

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W--> 59      (ii) MOLECULE TYPE: DNA
62      (ix) FEATURE:
63          (A) NAME/KEY: CDS
64          (B) LOCATION: 286..4386
67      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
69 TATAGGGCGA ATTGGGTACG GGACCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT      60
71 CGAATTCGGG CCCAGACTGT GTCCCGCAGC CGGGATAACC TGGCTGACCC GATTCCGCGG      120
73 ACACCGCTGA CAGCCGCGGC TGGAGCCAGG GCGCCGGTGC CCCGCGCTCT CCCCAGGTCTT      180
75 GCGCTGCGGG GGCCATACCG CCTCTGTGAC TTCTTTGCGG GCCAGGGACG GAGAAGGAGT      240
77 CTGTGCCTGA GAAACTGGGC TCTGTGCCCA GGCGCGAGGT GCAGG ATG GAG AGC      294
78                                     Met Glu Ser
79                                     1
81 AAG GCG CTG CTA GCT GTC GCT CTG TGG TTC TGC GTG GAG ACC CGA GCC      342
82 Lys Ala Leu Leu Ala Val Ala Leu Trp Phe Cys Val Glu Thr Arg Ala
83      5              10              15
85 GCC TCT GTG GGT TTG ACT GGC GAT TTT CTC CAT CCC CCC AAG CTC AGC      390
86 Ala Ser Val Gly Leu Thr Gly Asp Phe Leu His Pro Pro Lys Leu Ser
87 20              25              30              35
89 ACA CAG AAA GAC ATA CTG ACA ATT TTG GCA AAT ACA ACC CTT CAG ATT      438
90 Thr Gln Lys Asp Ile Leu Thr Ile Leu Ala Asn Thr Thr Leu Gln Ile
91              40              45              50
93 ACT TGC AGG GGA CAG CGG GAC CTG GAC TGG CTT TGG CCC AAT GCT CAG      486
94 Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro Asn Ala Gln
95              55              60              65
97 CGT GAT TCT GAG GAA AGG GTA TTG GTG ACT GAA TGC GGC GGT GGT GAC      534
98 Arg Asp Ser Glu Glu Arg Val Leu Val Thr Glu Cys Gly Gly Gly Asp
99      70              75              80
101 AGT ATC TTC TGC AAA ACA CTC ACC ATT CCC AGG GTG GTT GGA AAT GAT      582
102 Ser Ile Phe Cys Lys Thr Leu Thr Ile Pro Arg Val Val Gly Asn Asp
103      85              90              95
105 ACT GGA GCC TAC AAG TGC TCG TAC CGG GAC GTC GAC ATA GCC TCC ACT      630
106 Thr Gly Ala Tyr Lys Cys Ser Tyr Arg Asp Val Asp Ile Ala Ser Thr
107 100              105              110              115
109 GTT TAT GTC TAT GTT CGA GAT TAC AGA TCA CCA TTC ATC GCC TCT GTC      678
110 Val Tyr Val Tyr Val Arg Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val
111              120              125              130
113 AGT GAC CAG CAT GGC ATC GTG TAC ATC ACC GAG AAC AAG AAC AAA ACT      726
114 Ser Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys Asn Lys Thr
115              135              140              145
117 GTG GTG ATC CCC TGC CGA GGG TCG ATT TCA AAC CTC AAT GTG TCT CTT      774
118 Val Val Ile Pro Cys Arg Gly Ser Ile Ser Asn Leu Asn Val Ser Leu
119              150              155              160
121 TGC GCT AGG TAT CCA GAA AAG AGA TTT GTT CCG GAT GGA AAC AGA ATT      822
122 Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg Ile
123      165              170              175
125 TCC TGG GAC AGC GAG ATA GGC TTT ACT CTC CCC AGT TAC ATG ATC AGC      870
126 Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr Met Ile Ser
127 180              185              190              195
129 TAT GCC GGC ATG GTC TTC TGT GAG GCA AAG ATC AAT GAT GAA ACC TAT      918

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130	Tyr	Ala	Gly	Met	Val	Phe	Cys	Glu	Ala	Lys	Ile	Asn	Asp	Glu	Thr	Tyr	
131					200					205					210		
133	CAG	TCT	ATC	ATG	TAC	ATA	GTT	GTG	GTT	GTA	GGA	TAT	AGG	ATT	TAT	GAT	966
134	Gln	Ser	Ile	Met	Tyr	Ile	Val	Val	Val	Val	Gly	Tyr	Arg	Ile	Tyr	Asp	
135				215					220					225			
137	GTG	ATT	CTG	AGC	CCC	CCG	CAT	GAA	ATT	GAG	CTA	TCT	GCC	GGA	GAA	AAA	1014
138	Val	Ile	Leu	Ser	Pro	Pro	His	Glu	Ile	Glu	Leu	Ser	Ala	Gly	Glu	Lys	
139			230					235					240				
141	CTT	GTC	TTA	AAT	TGT	ACA	GCG	AGA	ACA	GAG	CTC	AAT	GTG	GGG	CTT	GAT	1062
142	Leu	Val	Leu	Asn	Cys	Thr	Ala	Arg	Thr	Glu	Leu	Asn	Val	Gly	Leu	Asp	
143		245					250					255					
145	TTC	ACC	TGG	CAC	TCT	CCA	CCT	TCA	AAG	TCT	CAT	CAT	AAG	AAG	ATT	GTA	1110
146	Phe	Thr	Trp	His	Ser	Pro	Pro	Ser	Lys	Ser	His	His	Lys	Lys	Ile	Val	
147	260					265				270						275	
149	AAC	CGG	GAT	GTG	AAA	CCC	TTT	CCT	GGG	ACT	GTG	GCG	AAG	ATG	TTT	TTG	1158
150	Asn	Arg	Asp	Val	Lys	Pro	Phe	Pro	Gly	Thr	Val	Ala	Lys	Met	Phe	Leu	
151				280					285					290			
153	AGC	ACC	TTG	ACA	ATA	GAA	AGT	GTG	ACC	AAG	AGT	GAC	CAA	GGG	GAA	TAC	1206
154	Ser	Thr	Leu	Thr	Ile	Glu	Ser	Val	Thr	Lys	Ser	Asp	Gln	Gly	Glu	Tyr	
155			295					300				305					
157	ACC	TGT	GTA	GCG	TCC	AGT	GGA	CGG	ATG	ATC	AAG	AGA	AAT	AGA	ACA	TTT	1254
158	Thr	Cys	Val	Ala	Ser	Ser	Gly	Arg	Met	Ile	Lys	Arg	Asn	Arg	Thr	Phe	
159			310				315					320					
161	GTC	CGA	GTT	CAC	ACA	AAG	CCT	TTT	ATT	GCT	TTC	GGT	AGT	GGG	ATG	AAA	1302
162	Val	Arg	Val	His	Thr	Lys	Pro	Phe	Ile	Ala	Phe	Gly	Ser	Gly	Met	Lys	
163		325				330						335					
165	TCT	TTG	GTG	GAA	GCC	ACA	GTG	GGC	AGT	CAA	GTC	CGA	ATC	CCT	GTG	AAG	1350
166	Ser	Leu	Val	Glu	Ala	Thr	Val	Gly	Ser	Gln	Val	Arg	Ile	Pro	Val	Lys	
167	340				345				350					355			
169	TAT	CTC	AGT	TAC	CCA	GCT	CCT	GAT	ATC	AAA	TGG	TAC	AGA	AAT	GGA	AGG	1398
170	Tyr	Leu	Ser	Tyr	Pro	Ala	Pro	Asp	Ile	Lys	Trp	Tyr	Arg	Asn	Gly	Arg	
171				360					365					370			
173	CCC	ATT	GAG	TCC	AAC	TAC	ACA	ATG	ATT	GTT	GGC	GAT	GAA	CTC	ACC	ATC	1446
174	Pro	Ile	Glu	Ser	Asn	Tyr	Thr	Met	Ile	Val	Gly	Asp	Glu	Leu	Thr	Ile	
175			375					380				385					
177	ATG	GAA	GTG	ACT	GAA	AGA	GAT	GCA	GGA	AAC	TAC	ACG	GTC	ATC	CTC	ACC	1494
178	Met	Glu	Val	Thr	Glu	Arg	Asp	Ala	Gly	Asn	Tyr	Thr	Val	Ile	Leu	Thr	
179			390				395					400					
181	AAC	CCC	ATT	TCA	ATG	GAG	AAA	CAG	AGC	CAC	ATG	GTC	TCT	CTG	GTT	GTG	1542
182	Asn	Pro	Ile	Ser	Met	Glu	Lys	Gln	Ser	His	Met	Val	Ser	Leu	Val	Val	
183		405				410					415						
185	AAT	GTC	CCA	CCC	CAG	ATC	GGT	GAG	AAA	GCC	TTG	ATC	TCG	CCT	ATG	GAT	1590
186	Asn	Val	Pro	Pro	Gln	Ile	Gly	Glu	Lys	Ala	Leu	Ile	Ser	Pro	Met	Asp	
187	420				425				430				435				
189	TCC	TAC	CAG	TAT	GGG	ACC	ATG	CAG	ACA	TTG	ACA	TGC	ACA	GTC	TAC	GCC	1638
190	Ser	Tyr	Gln	Tyr	Gly	Thr	Met	Gln	Thr	Leu	Thr	Cys	Thr	Val	Tyr	Ala	
191			440					445				450					
193	AAC	CCT	CCC	CTG	CAC	CAC	ATC	CAG	TGG	TAC	TGG	CAG	CTA	GAA	GAA	GCC	1686
194	Asn	Pro	Pro	Leu	His	His	Ile	Gln	Trp	Tyr	Trp	Gln	Leu	Glu	Glu	Ala	

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195				455					460					465					
197	TGC	TCC	TAC	AGA	CCC	GGC	CAA	ACA	AGC	CCG	TAT	GCT	TGT	AAA	GAA	TGG	1734		
198	Cys	Ser	Tyr	Arg	Pro	Gly	Gln	Thr	Ser	Pro	Tyr	Ala	Cys	Lys	Glu	Trp			
199	470			475					480										
201	AGA	CAC	GTG	GAG	GAT	TTC	CAG	GGG	GGA	AAC	AAG	ATC	GAA	GTC	ACC	AAA	1782		
202	Arg	His	Val	Glu	Asp	Phe	Gln	Gly	Gly	Asn	Lys	Ile	Glu	Val	Thr	Lys			
203	485			490					495										
205	AAC	CAA	TAT	GCC	CTG	ATT	GAA	GGA	AAA	AAC	AAA	ACT	GTA	AGT	ACG	CTG	1830		
206	Asn	Gln	Tyr	Ala	Leu	Ile	Glu	Gly	Lys	Asn	Lys	Thr	Val	Ser	Thr	Leu			
207	500			505					510					515					
209	GTC	ATC	CAA	GCT	GCC	AAC	GTG	TCA	GCG	TTG	TAC	AAA	TGT	GAA	GCC	ATC	1878		
210	Val	Ile	Gln	Ala	Ala	Asn	Val	Ser	Ala	Leu	Tyr	Lys	Cys	Glu	Ala	Ile			
211				520					525					530					
213	AAC	AAA	GCG	GGA	CGA	GGA	GAG	AGG	GTC	ATC	TCC	TTC	CAT	GTG	ATC	AGG	1926		
214	Asn	Lys	Ala	Gly	Arg	Gly	Glu	Arg	Val	Ile	Ser	Phe	His	Val	Ile	Arg			
215				535					540					545					
217	GGT	CCT	GAA	ATT	ACT	GTG	CAA	CCT	GCT	GCC	CAG	CCA	ACT	GAG	CAG	GAG	1974		
218	Gly	Pro	Glu	Ile	Thr	Val	Gln	Pro	Ala	Ala	Gln	Pro	Thr	Glu	Gln	Glu			
219	550			555					560										
221	AGT	GTG	TCC	CTG	TTG	TGC	ACT	GCA	GAC	AGA	AAT	ACG	TTT	GAG	AAC	CTC	2022		
222	Ser	Val	Ser	Leu	Leu	Cys	Thr	Ala	Asp	Arg	Asn	Thr	Phe	Glu	Asn	Leu			
223	565			570					575										
225	ACG	TGG	TAC	AAG	CTT	GGC	TCA	CAG	GCA	ACA	TCG	GTC	CAC	ATG	GGC	GAA	2070		
226	Thr	Trp	Tyr	Lys	Leu	Gly	Ser	Gln	Ala	Thr	Ser	Val	His	Met	Gly	Glu			
227	580			585					590					595					
229	TCA	CTC	ACA	CCA	GTT	TGC	AAG	AAC	TTG	GAT	GCT	CTT	TGG	AAA	CTG	AAT	2118		
230	Ser	Leu	Thr	Pro	Val	Cys	Lys	Asn	Leu	Asp	Ala	Leu	Trp	Lys	Leu	Asn			
231				600					605					610					
233	GGC	ACC	ATG	TTT	TCT	AAC	AGC	ACA	AAT	GAC	ATC	TTG	ATT	GTG	GCA	TTT	2166		
234	Gly	Thr	Met	Phe	Ser	Asn	Ser	Thr	Asn	Asp	Ile	Leu	Ile	Val	Ala	Phe			
235				615					620					625					
237	CAG	AAT	GCC	TCT	CTG	CAG	GAC	CAA	GGC	GAC	TAT	GTT	TGC	TCT	GCT	CAA	2214		
238	Gln	Asn	Ala	Ser	Leu	Gln	Asp	Gln	Gly	Asp	Tyr	Val	Cys	Ser	Ala	Gln			
239	630			635					640										
241	GAT	AAG	AAG	ACC	AAG	AAA	AGA	CAT	TGC	CTG	GTC	AAA	CAG	CTC	ATC	ATC	2262		
242	Asp	Lys	Lys	Thr	Lys	Lys	Arg	His	Cys	Leu	Val	Lys	Gln	Leu	Ile	Ile			
243	645			650					655										
245	CTA	GAG	CGC	ATG	GCA	CCC	ATG	ATC	ACC	GGA	AAT	CTG	GAG	AAT	CAG	ACA	2310		
246	Leu	Glu	Arg	Met	Ala	Pro	Met	Ile	Thr	Gly	Asn	Leu	Glu	Asn	Gln	Thr			
247	660			665					670					675					
249	ACA	ACC	ATT	GGC	GAG	ACC	ATT	GAA	GTG	ACT	TGC	CCA	GCA	TCT	GGA	AAT	2358		
250	Thr	Thr	Ile	Gly	Glu	Thr	Ile	Glu	Val	Thr	Cys	Pro	Ala						

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261	AGG	GTG	AGG	AAG	GAG	GAT	GGA	GGC	CTC	TAC	ACC	TGC	CAG	GCC	TGC	AAT	2502
262	Arg	Val	Arg	Lys	Glu	Asp	Gly	Gly	Leu	Tyr	Thr	Cys	Gln	Ala	Cys	Asn	
263		725					730					735					
265	GTC	CTT	GGC	TGT	GCA	AGA	GCG	GAG	ACG	CTC	TTC	ATA	ATA	GAA	GGT	GCC	2550
266	Val	Leu	Gly	Cys	Ala	Arg	Ala	Glu	Thr	Leu	Phe	Ile	Ile	Glu	Gly	Ala	
267	740					745				750						755	
269	CAG	GAA	AAG	ACC	AAC	TTG	GAA	GTC	ATT	ATC	CTC	GTC	GGC	ACT	GCA	GTG	2598
270	Gln	Glu	Lys	Thr	Asn	Leu	Glu	Val	Ile	Ile	Leu	Val	Gly	Thr	Ala	Val	
271					760					765						770	
273	ATT	GCC	ATG	TTC	TTC	TGG	CTC	CTT	CTT	GTC	ATT	GTC	CTA	CGG	ACC	GTT	2646
274	Ile	Ala	Met	Phe	Phe	Trp	Leu	Leu	Leu	Val	Ile	Val	Leu	Arg	Thr	Val	
275				775						780						785	
277	AAG	CGG	GCC	AAT	GAA	GGG	GAA	CTG	AAG	ACA	GGC	TAC	TTG	TCT	ATT	GTC	2694
278	Lys	Arg	Ala	Asn	Glu	Gly	Glu	Leu	Lys	Thr	Gly	Tyr	Leu	Ser	Ile	Val	
279			790						795				800				
281	ATG	GAT	CCA	GAT	GAA	TTG	CCC	TTG	GAT	GAG	CGC	TGT	GAA	CGC	TTG	CCT	2742
282	Met	Asp	Pro	Asp	Glu	Leu	Pro	Leu	Asp	Glu	Arg	Cys	Glu	Arg	Leu	Pro	
283		805					810						815				
285	TAT	GAT	GCC	AGC	AAG	TGG	GAA	TTC	CCC	AGG	GAC	CGG	CTG	AAA	CTA	GGA	2790
286	Tyr	Asp	Ala	Ser	Lys	Trp	Glu	Phe	Pro	Arg	Asp	Arg	Leu	Lys	Leu	Gly	
287	820					825					830					835	
289	AAA	CCT	CTT	GGC	CGC	GGT	GCC	TTC	GGC	CAA	GTG	ATT	GAG	GCA	GAC	GCT	2838
290	Lys	Pro	Leu	Gly	Arg	Gly	Ala	Phe	Gly	Gln	Val	Ile	Glu	Ala	Asp	Ala	
291					840					845						850	
293	TTT	GGA	ATT	GAC	AAG	ACA	GCG	ACT	TGC	AAA	ACA	GTA	GCC	GTC	AAG	ATG	2886
294	Phe	Gly	Ile	Asp	Lys	Thr	Ala	Thr	Cys	Lys	Thr	Val	Ala	Val	Lys	Met	
295				855						860						865	
297	TTG	AAA	GAA	GGA	GCA	ACA	CAC	AGC	GAG	CAT	CGA	GCC	CTC	ATG	TCT	GAA	2934
298	Leu	Lys	Glu	Gly	Ala	Thr	His	Ser	Glu	His	Arg	Ala	Leu	Met	Ser	Glu	
299			870						875					880			
301	CTC	AAG	ATC	CTC	ATC	CAC	ATT	GGT	CAC	CAT	CTC	AAT	GTG	GTG	AAC	CTC	2982
302	Leu	Lys	Ile	Leu	Ile	His	Ile	Gly	His	His	Leu	Asn	Val	Val	Asn	Leu	
303		885					890						895				
305	CTA	GGC	GCC	TGC	ACC	AAG	CCG	GGA	GGG	CCT	CTC	ATG	GTG	ATT	GTG	GAA	3030
306	Leu	Gly	Ala	Cys	Thr	Lys	Pro	Gly	Gly	Pro	Leu	Met	Val	Ile	Val	Glu	
307	900					905					910					915	
309	TTC	TGC	AAG	TTT	GGA	AAC	CTA	TCA	ACT	TAC	TTA	CGG	GGC	AAG	AGA	AAT	3078
310	Phe	Cys	Lys	Phe	Gly	Asn	Leu	Ser	Thr	Tyr	Leu	Arg	Gly	Lys	Arg	Asn	
311					920					925						930	
313	GAA	TTT	GTT	CCC	TAT	AAG	AGC	AAA	GGG	GCA	CGC	TTC	CGC	CAG	GGC	AAG	3126
314	Glu	Phe	Val	Pro	Tyr	Lys	Ser	Lys	Gly	Ala	Arg	Phe	Arg	Gln	Gly	Lys	
315				935						940						945	
317	GAC	TAC	GTT	GGG	GAG	CTC	TCC	GTG	GAT	CTG	AAA	AGA	CGC	TTG	GAC	AGC	3174
318	Asp	Tyr	Val	Gly	Glu	Leu	Ser	Val	Asp	Leu	Lys	Arg	Arg	Leu	Asp	Ser	
319			950						955							960	
321	ATC	ACC	AGC	AGC	CAG	AGC	TCT	GCC	AGC	TCA	GGC	TTT	GTT	GAG	GAG	AAA	3222
322	Ile	Thr	Ser	Ser	Gln	Ser	Ser	Ala	Ser	Ser	Gly	Phe	Val	Glu	Glu	Lys	
323		965					970						975				
325	TCG	CTC	AGT	GAT	GTA	GAG	GAA	GAA	GAA	GCT	TCT	GAA	GAA	CTG	TAC	AAG	3270

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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:59 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:740 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:756 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4